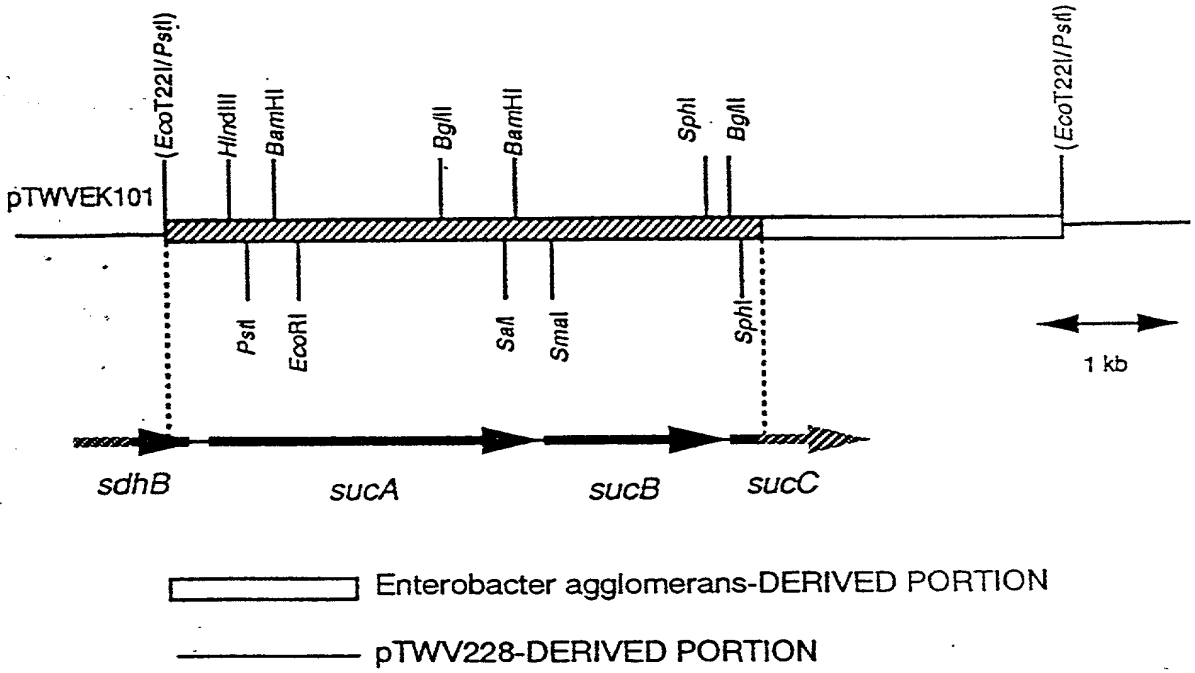

(EcoT22I/PstI)
HindIII
BamHI
BglII
BamHI
SphI
BglII
(EcoT22I/PstI)
pTWVEK101
PstI
EcoRI
SalI
SmaI
SphI
1 kb
sdhB
sucA
sucB
sucC
Enterobacter agglomerans-DERIVED PORTION
pTWV228-DERIVED PORTION

FIG. 1

[88.0% / 935 aa]

```
  1' MQNSAMKPWLDSSWLAGANQSYIEQLYEDFLTDPDSVDAVWRSMFQQLPGTGVKPEQFHS
     ***** * ***** * ***** ********** *** ********** ****
  1" MQNSALKAWLDSSYLSGANQSWIEQLYEDFLTDPDSVDANWRSTFQQLPGTGVKPDQFHS

 61' ATREYFRRLAKDASRYTSSVTDPATNSKQVKVLQLINAFRFRGHQEANLDPLGLWKQDRV
     ********** * .. ** ** ********** ****** ********* ** *
 61" QTREYFRRLAKDASRYSSTISDPDTNVKQVKVLQLINAYRFRGHQHANLDPLGLWQQDKV

121' ADLDPAFHDLTDADFQESFNVGSFAIGKETMKLADLFDALKQTYCGSIGAEYMHINNTEE
     ***** ***** ***** ******* ******* * ******** ******** ***
121" ADLDPSFHDLTEADFQETFNVGSFASGKETMKLGELLEALKQTYCGPIGAEYMHITSTEE

181' KRWIQQRIESGASQTSFSGEEKKGFLKELTAAEGLEKYLGAKFPGAKRFSLEGGDALVPM
     ********** ... * .. **** ** ********* ********** ** **
181" KRWIQQRIESG--RATFNSEEKKRFLSELTAAEGLERYLGAKFPGAKRFSLEGGDALIPM

241' LREMIRHAGKSGTREVVLGMAHRGRLNVLINVLGKKPQDLFDEFSGKHKEHLGTGDVKYH
     * ******* ********** ********** **********
239" LKEMIRHAGNSGTREVVLGMAHRGRLNVLVNVLGKKPQDLFDEFAGKHKEHLGTGDVKYH

301' MGFSSDIETEGGLVHLALAFNPSHLEIVSPVVMGSVRARLDRLAEPVSNKVLPITIHGDA
     ****** .. * ********** ********** ** **********
299" MGFSSDFQTDGGLVHLALAFNPSHLEIVSPVVIGSVRARLDRLDEPSSNKVLPITIHGDA

361' AVIGQGVVQETLNMSQARGYEVGGTVRIVINNQVGFTTSNPKDARSTPYCTDIGKMVLAP
     ** ********** ********** ********** ** **
359" AVTGQGVVQETLNMSKARGYEVGGTVRIVINNQVGFTTSNPLDARSTPYCTDIGKMVQAP

421' IFHVNADDPEAVAFVTRLALDYRNTFKRDVFIDLVCYRRHGHNEADEPSATQPLMYQKIK
     ********** ********** **********
419" IFHVNADDPEAVAFVTRLALDFRNTFKRDVFIDLVSYRRHGHNEADEPSATQPLMYQKIK

481' KHPTPRKIYADRLEGEGVASQEDATEMVNLYRDALDAGECVVPEWRPMSLHSFTWSPYLN
     ********** ** * ** ********** *** ***** **********
479" KHPTPRKIYADKLEQEKVATLEDATEMVNLYRDALDAGDCVVAEWRPMNMHSFTWSPYLN

541' HEWDEPYPAQVDMKRLKELALRISQVPEQIEVQSRVAKIYNDRKLMAEGEKAFDWGGAEN
     ***** ** . * **** *** *** *** . * ******** ** ** *** ********
539" HEWDEEYPNKVEMKRLQELAKRISTVPEAVEMQSRVAKIYGDRQAMAAGEKLFDWGGAEN

601' LAYATLVDEGIPVRLSGEDSGRGTFFHRHAVVHNQANGSTYTPLHHIHNSQGEFKVWDSV
     ********** *** ******** **** ** * ******
599" LAYATLVDEGIPVRLSGEDSGRGTFFHRHAVIHNQSNGSTYTPLQHIHNGQGAFRVWDSV

661' LSEEAVLAFEYGYATAEPRVLTIWEAQFGDFANGAQVVIDQFISSGEQKWGRMCGLVMLL
     ********** ********** **********
659" LSEEAVLAFEYGYATAEPRTLTIWEAQFGDFANGAQVVIDQFISSGEQKWGRMCGLVMLL

721' PHGYEGQGPEHSSARLERYLQLCAEQNMQVCVPSTPAQVYHMLRRQALRGMRRPLVVMSP
     **********
719" PHGYEGQGPEHSSARLERYLQLCAEQNMQVCVPSTPAQVYHMLRRQALRGMRRPLVVMSP

781' KSLLRHPLAISSLDELANGSFQPAIGEIDDLDPQGVKRVVLCSGKVYYDLLEQRRKDEKT
     ********** *** ****** * ******* *** ****** **********
779" KSLLRHPLAVSSLEELANGTFLPAIGEIDELDPKGVKRVVMCSGKVYYDLLEQRRKNNQH

841' DVAIVRIEQLYPFPHQAVQEALKAYSHVQDFVWCQEEPLNQGAWYCSQHHFRDVVPFGAT
     ********** * ** * .... ** ********** * * *****
839" DVAIVRIEQLYPFPHKAMQEVLQQFAHVKDFVWCQEEPLNQGAWYCSQHHFREVIPFGAS

901' LRYAGRPASASPAVGYMSVHQQQQQDLVNDALNVN
     ********** **********
899" LRYAGRPASASPAVGYMSVHQKQQQDLVNDALNVE
```

FIG. 2

[88.2% / 407 aa]

```
    1' MSSVDILVPDLPESVADATVATWHKKPGDAVSRDEVIVEIETDKVVLEVPASADGVLEAV
       ********************************* **** ********************.*.**
    1" MSSVDILVPDLPESVADATVATWHKKPGDAVVRDEVLVEIETDKVVLEVPASADGILDAV

   61' LEDEGATVTSRQILGRLKEGNSAGKESSAKAESNDTTPAQRQTASLEEESSDALSPAIRR
       ***** ********** ******** *** * .... ****** ****** ... *********
   61" LEDEGTTVTSRQILGRLREGNSAGKETSAKSEEKASTPAQRQQASLEEQNNDALSPAIRR

  121' LIAEHNLDAAQIKGTGVGGRLTREDVEKHLANKPQAEKAAAPAAGAATAQQPVANRSEKR
       * ******** ********************* * * * .**** * .. ** ... * *****
  121" LLAEHNLDASAIKGTGVGGRLTREDVEKHLAKAPAKE--SAPAAAAPAAQPALAARSEKR

  181' VPMTRLRKRVAERLLEAKNSTAMLTTFNEINMKPIMDLRKQYGDAFEKRHGVRLGFMSFY
       ************************ ******* ************ ******* ********
  179" VPMTRLRKRVAERLLEAKNSTAMLTTFNEVNMKPIMDLRKQYGEAFEKRHGIRLGFMSFY

  241' IKAVVEALKRYPEVNASIDGEDVVYHNYFDVSIAVSTPRGLVTPVLRDVDALSMADIEKK
       ********************* ********** ***************** * ********
  239" VKAVVEALKRYPEVNASIDGDDVVYHNYFDVSMAVSTPRGLVTPVLRDVDTLGMADIEKK

  301' IKELAVKGRDGKLTVDDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAV
       *************** ************************************************
  299" IKELAVKGRDGKLTVEDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAV

  361' NGQVVILPMMYLALSYDHRLIDGRESVGYLVAVKEMLEDPARLLLDV
       **** ********************** ** .. ** .**** .******
  359" NGQVEILPMMYLALSYDHRLIDGRESVGFLVTIKELLEDPTRLLLDV
```

FIG. 3

[95.1% / 41 aa]

```
    1' MNLHEYQAKQLFARYGMPAPTGYACTTPREAEEAASKIGAG
       ***************** *** ********************
    1" MNLHEYQAKQLFARYGLPAPVGYACTTPREAEEAASKIGAGPWVVKCQVHAGGRGKAGGV
```

FIG. 4

[97.4% / 39 aa]

```
    1'                      AFSVFRCHSIMNCVSVCPKGLNPTRAIGHIKSMLLQRSA
                            ************************************ *
  181" FLIDSRDTETDSRLDGLSDAFSVFRCHSIMNCVSVCPKGLNPTRAIGHIKSMLLQRNA
```

FIG. 5

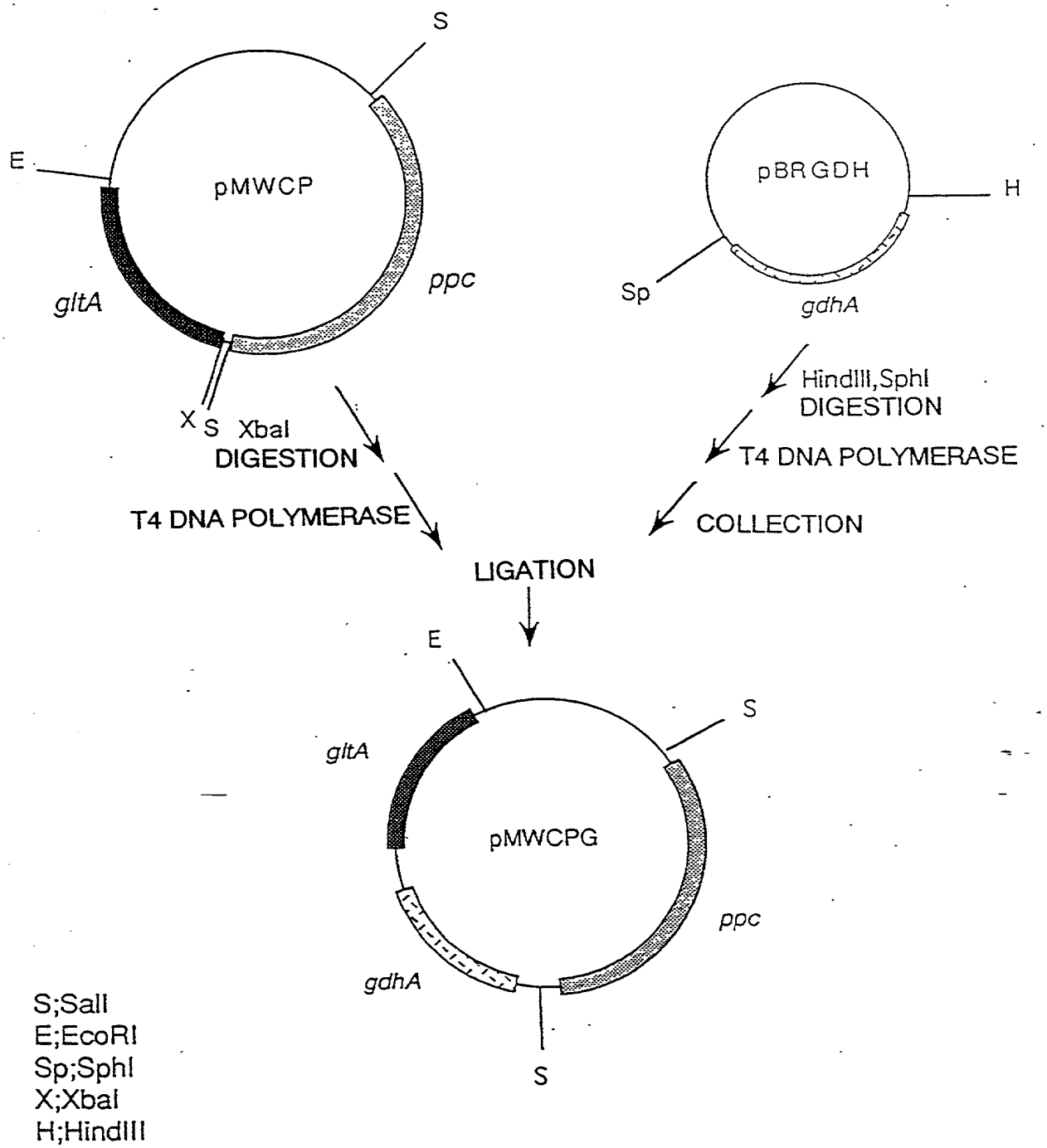

S
E
pMWCP
gltA
ppc
X
S
XbaI
DIGESTION
T4 DNA POLYMERASE
pBRGDH
H
Sp
gdhA
HindIII,SphI
DIGESTION
T4 DNA POLYMERASE
COLLECTION
LIGATION
E
S
gltA
pMWCPG
ppc
gdhA
S
S;SalI
E;EcoRI
Sp;SphI
X;XbaI
H;HindIII

FIG. 6

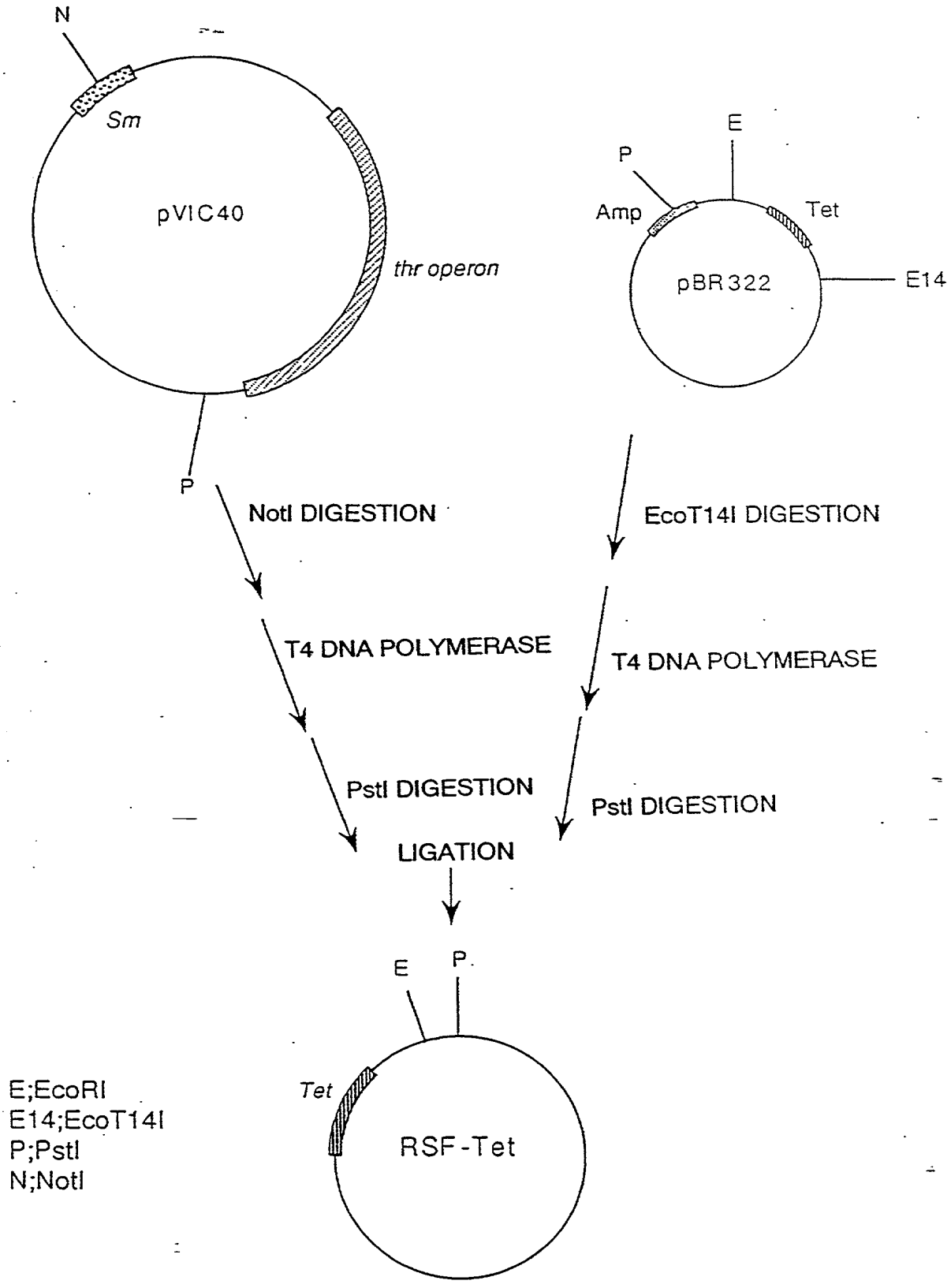
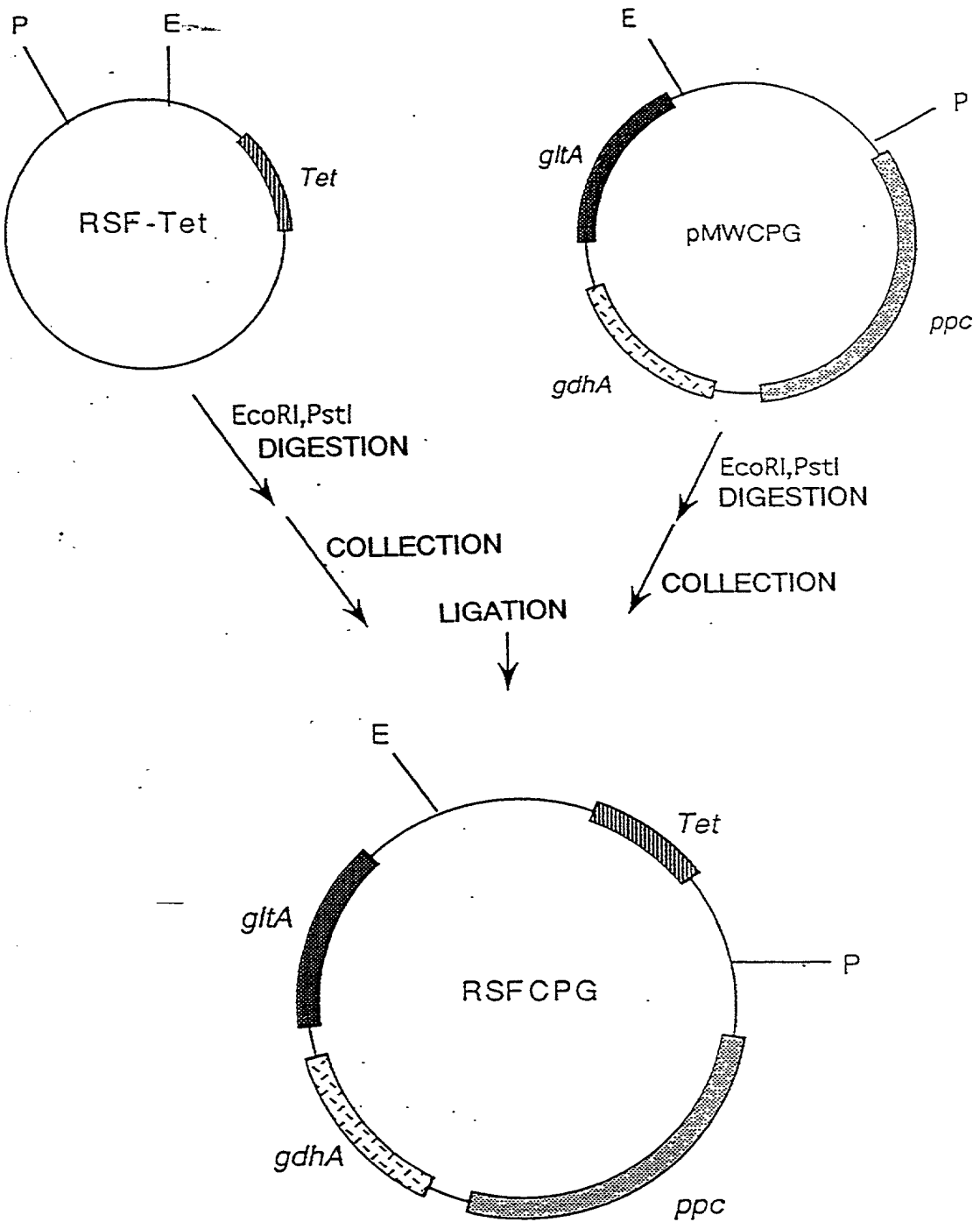

N
Sm
pVIC40
thr operon
P
E
P
Amp
Tet
pBR322
E14
NotI DIGESTION
EcoT14I DIGESTION
T4 DNA POLYMERASE
T4 DNA POLYMERASE
PstI DIGESTION
PstI DIGESTION
LIGATION
E
P
Tet
RSF-Tet
E;EcoRI
E14;EcoT14I
P;PstI
N;NotI

FIG. 7



E;EcoRI
P;PstI

FIG. 8

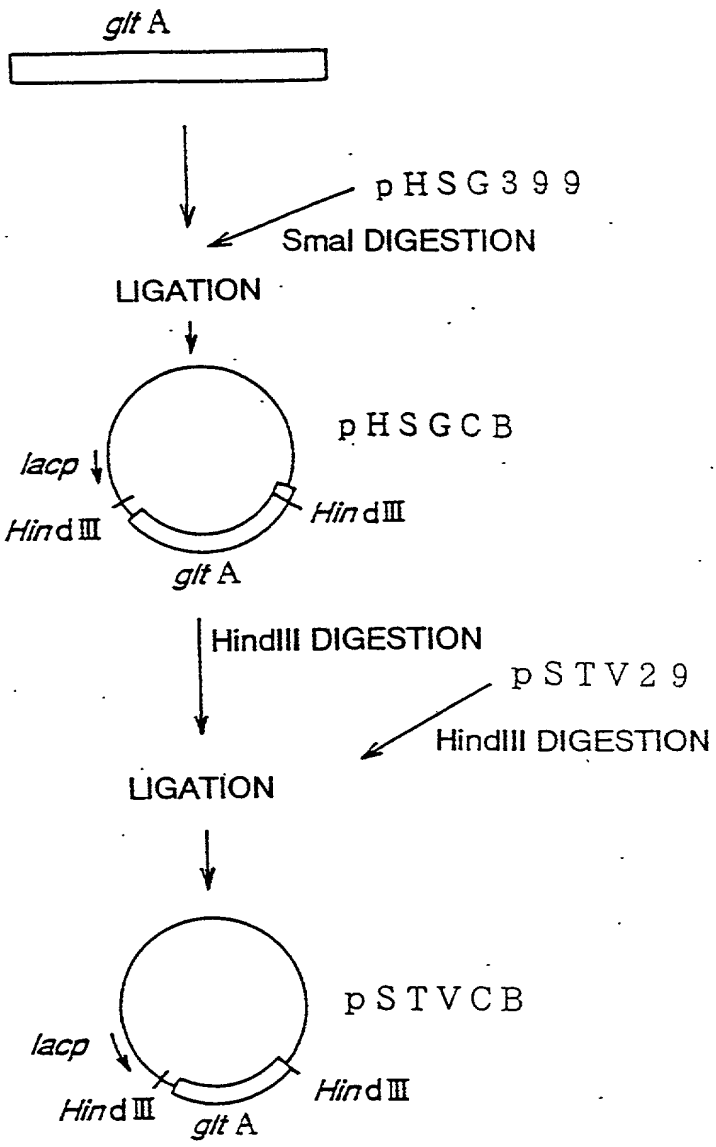

glt A
pHSG399
SmaI DIGESTION
LIGATION
pHSGCB
lacp
HindIII
HindIII
glt A
HindIII DIGESTION
pSTV29
HindIII DIGESTION
LIGATION
pSTVCB
lacp
HindIII
HindIII
glt A

FIG. 9